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 NEWS  2          "Ask CAS" for self-help around the clock
 NEWS  3  SEP 09  CA/CAplus records now contain indexing from 1907 to the
                  present
 NEWS  4  DEC 08  INPADOC: Legal Status data reloaded
 NEWS  5  SEP 29  DISSABS now available on STN
 NEWS  6  OCT 10  PCTFULL: Two new display fields added
 NEWS  7  OCT 21  BIOSIS file reloaded and enhanced
 NEWS  8  OCT 28  BIOSIS file segment of TOXCENTER reloaded and enhanced
 NEWS  9  NOV 24  MSDS-CCOHS file reloaded
 NEWS 10  DEC 08  CABA reloaded with left truncation
 NEWS 11  DEC 08  IMS file names changed
 NEWS 12  DEC 09  Experimental property data collected by CAS now available
                  in REGISTRY
 NEWS 13  DEC 09  STN Entry Date available for display in REGISTRY and CA/CAplus
 NEWS 14  DEC 17  DGENE: Two new display fields added
 NEWS 15  DEC 18  BIOTECHNO no longer updated
 NEWS 16  DEC 19  CROPU no longer updated; subscriber discount no longer
                  available
 NEWS 17  DEC 22  Additional INPI reactions and pre-1907 documents added to CAS
                  databases
 NEWS 18  DEC 22  IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22  ABI-INFORM now available on STN
 NEWS 20  JAN 27  Source of Registration (SR) information in REGISTRY updated
                  and searchable
 NEWS 21  JAN 27  A new search aid, the Company Name Thesaurus, available in
                  CA/CAplus
 NEWS 22  FEB 05  German (DE) application and patent publication number format
                  changes

 NEWS EXPRESS  DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
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L2    ANSWER 1 OF 2  BIOTECHABS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
AN    1988-03786  BIOTECHABS
TI    Protein crystallography;
        and its application to protein engineering
AU    Janin J
LO    Laboratoire de Biologie Physicochimique, Universite Paris-Sud, Orsay,
      France.
SO    Biofutur; (1987) 62, 29-31
DT    Journal
LA    French
AB    X-ray diffraction remains the only technique capable of resolving the
      structure of biological macromolecules at atomic detail.  The major
      difficulties in the technique remain the preparation of adequate
      crystalline samples and the determination of the phase of diffracted
      rays.  In recent years progress has come from the use of synchrotrons as
      X-ray sources of high intensity which has speeded up the rate of data
      capture and has made possible the resolution by X-ray diffraction of
      movements within macromolecules.  The precision of the map of electron
      density provided by the technique is usually of the order of 0.2-0.3 nm,
      but methods are available which permit resolutions of 0.01 nm: resolution
      at this level is sometimes necessary to determine catalytic mechanisms
      and the precise position of ligands.  Protein crystallography
      remains a somewhat unpredictable undertaking, but it is an
      irreplaceable resource for the developing field of protein engineering.
      (4 ref)

L2   ANSWER 2 OF 2  USPATFULL on STN
AN     2002:335702  USPATFULL
TI     High-throughput biomolecular crystallization and biomolecular crystal
       screening
IN     Mutz, Mitchell W., Palo Alto, CA, UNITED STATES
       Ellson, Richard N., Palo Alto, CA, UNITED STATES
       Stearns, Richard G., Felton, CA, UNITED STATES
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PI US 2002191048 A1 20021219
AI US 2002-55245 A1 20020122 (10)
RLI Continuation-in-part of Ser. No. US 2001-765947, filed on 19 Jan 2001, PENDING Continuation-in-part of Ser. No. US 2000-727392, filed on 29 Nov 2000, PENDING Continuation-in-part of Ser. No. US 2000-669996, filed on 25 Sep 2000, PENDING
DT Utility
FS APPLICATION
LREP REED & ASSOCIATES, 800 MENLO AVENUE, SUITE 210, MENLO PARK, CA, 94025
CLMN Number of Claims: 150
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 3490
AB The present invention provides a method for the acoustic ejection of fluid droplets from fluid-containing reservoirs to form arrays suitable for high-throughput combinatorial crystallization experiments. Such arrays may utilize very small fluid volumes, in the order of picoliters. The method is especially suited to preparing combinatorial libraries useful in developing techniques for crystallizing biomacromolecules, such as proteins. The small volumes conserve macromolecules that may be costly and rare, and permit the testing of a large number of experimental crystallization conditions for a given amount of a macromolecule. The time required for the experiments may be very short due to the small volumes. The invention is conducive to forming high-density microarrays of small volume crystallization experiments. Acoustic detection of crystals in situ, and distinction between biomacromolecular and non-biomacromolecular crystals, are also taught.